

SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANT: Bidwell, Christopher A.
Spurlock, Michael E.
- (ii) TITLE OF INVENTION: PORCINE LEPTIN PROTEIN, NUCLEIC ACID
SEQUENCES CODING THEREFOR AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: WHYTE HIRSCHBOECK DUDEK S.C.
 - (B) STREET: Suite 2100 111 East Wisconsin Avenue
 - (C) CITY: Milwaukee
 - (D) STATE: Wisconsin
 - (E) COUNTRY: USA
 - (F) ZIP: 53202
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/692,922
 - (B) FILING DATE: 31-JUL-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Shaw, Melissa A.
 - (B) REGISTRATION NUMBER: 38,301
 - (C) REFERENCE/DOCKET NUMBER: PM-8935
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 414-273-2100
 - (B) TELEFAX: 414-223-5000

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5917 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: join(942..1085, 3400..3753)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGCTTTCTT GGCCCCTAAC AGCAACCACA TTATACTCTT ACTGGCTATT CCTTGGCCTT	60
CAATACCCAG CCCAGGGGAC CCCTCTTCCA GGGAGCCCCG CTTGTACTCC TGAGATGTCA	120
TGTCCTTCTT GCAGAGCTCT TCCTCACGGC ATCGGGACGG CGGTTACACC TTTTGCCTCT	180

CCGGATAAAC TGTAAGCTAC TTGAGAGCAG AGAACATCCA TTGTTGCTG TGGCATCCGT	240
GGTACCTAGC ACGGCATCTG ACATATTATC AGATCTTCCA CAAAGGCCAG TTTACGGTTG	300
AATGCCCGTT GAATTCAGGC TCCCAGTGGG AGAGCGAGGA AGTAATAAAG CCGGTGATAA	360
ATGCCGCCGT GGAGACACCA GCGGGCTGCC GTGAGACTAA TGGAGAGGAC AGTAACGTTA	420
TCTCTAATGC GAGGGTGGTT ATAGAGTACA TTTCATAACA CCTTTAAAGC TCTTTCACAC	480
GCATTATCCA ATTTGATCCT CATAAAAGCC TGGAGATGTG TATATTGTGG TGGATGGAGG	540
GGGAGTCTTT AGCAGTTATG GGATATGCCT GAAGTCGTGC AGCTAGTAAA TGGCTGGATT	600
CAAACCAGAC CTCAAAAGCC TGCTGTGTTG CTCATGCCCC CTGCCCCGAC TGCCCACTCT	660
GTGGCCCCACA GCACAACTCA CCGTCGCTTT CTTGATCCGT TTTCTTGATC CGGCTGTGCT	720
CTCCCCAAGG AATGCTTTTC ATTAACATAT GTCTAGGTAA TGAATTATCT TGAATCTGAG	780
GAGGCCATAG CACATGCCGT AACGCGACAG CTCCTTTGAT CTGCATCTGA GGCTGTGGCT	840
GGTAACGGGC GTGGGGAGGG GCGTTCGCT GAGACCCAG GGACACGCCA TGTGTGGTTC	900
CCTCTGTTTC CAGGCCCCAG AAGCACATCC CGGAAAGGAA A ATG CGC TGT GGA	953
Met Arg Cys Gly	
1	
CCC CTG TGC CGA TTC CTG CTG GCT TTG GCC TAT CTG TCC TAC GTT GAA	1001
Pro Leu Cys Arg Phe Leu Leu Ala Leu Ala Tyr Leu Ser Tyr Val Glu	
5 10 15 20	
GCC GTG CCC ATC TGG AGA GTC CAG GAT GAC ACC AAA ACC CTC ATC AAG	1049
Ala Val Pro Ile Trp Arg Val Gln Asp Asp Thr Lys Thr Leu Ile Lys	
25 30 35	
ACG ATT GTC ACC AGG ATC AGT GAC ATT TCA CAC ATG GTAGGGAAGG	1095
Thr Ile Val Thr Arg Ile Ser Asp Ile Ser His Met	
40 45	
CCTGGGAGAC AAGGTCGAAC CTGTGGCCAG CCCSGGGGGA GGAGGGGTAC CGGACCTCAG	1155
AGGTGCGCGG AGGTGGGAAG GGTCGGCGGT GGCCTTGACG CCTCCCCAC CCCCCCAAC	1215
CAGTGCCCTT TGCTCCTCCG CTTCCCTCAC CGCACCCCC CACGTCCTTA TCCTCCTTCT	1275
TCCCAGACTG GAATCCTGAT GCCCAGGACT AGAGGAAGCC CTAAAGGTCC TGTGTGCCTT	1335
TGCCAGGTGC GCAGACCCCC CAGCATCATC CCCTCTGGCC TCCATCACGT CTCCGGAATG	1395
TTCTAATCTG TAGGAATTCT TCCTGGTGAC AGCTGAACTC TGACCCTGCG GACGCCCCCT	1455
ACTGCTAGTC CTGCCCATTG AGCCTTTTTT CCTATACAAC CCTCTACATG TTTGCAAACT	1515
TCTCTCAATG TCCCCAGGGT GTTTTCTCTG GGGTCCGCAG GCCGAGACCT TCAGCCTCTT	1575
CTCAGCTGAG GTCCGTCTTT AGAATTCAGA AGACGAGGTG TGAATCCTCA CCCTGCTGTT	1635
CCCTCTCTGT AAAATCTCAA GCACGTTAAG TCCCTCCGTG TCTGAAACCT TAGTTTCCCT	1695
CATCCAGATA ATGGGACTGT TACTGGGAAG ATGTTACCGG AATCCAGGGT CTTGCCTCAT	1755
GGAGCTCAAG AATGAACCTG GCGAACGCAC AGGGAGCCGA GCAAGCAGAA GTCTTTATTA	1815

CAGGAAGGCA GACAGCTCCC AGCACAGACA CGGGGAGGGA AGAGTCCCC CGCCCATTTGT	1875
TCTACGGAGG TTTTATCAC TTAAAGACGG GAGTACCAAT GTGGGGTCCA GATATCCGTT	1935
CTTCTTCCCA TTGCCCAGTT TACCTATATG GCGCCTTGTC CAGGAGGGAC TCTGTAGAGT	1995
TAGGGGTGCT CCGTAAGTTT TATGGTGCGT CTGCTCTTCT CTGCCCTAGA CTTAGAGTCG	2055
CCACTCTTTC CATTCTTCTG CTCACAGTCA AATGCATAGG TCAGGGGTTA ATTCCACCT	2115
TCACAGAAAT CAAATGTCCT TTCAATAGTT AATCTTCCAA TAAGCAAGGC CTGCTTGTCT	2175
TGATTAGTTT TTACAAATCT TAAACCATGG CCATTAATCA GGGAAGAGAT CGAAGCCCAT	2235
GTTCCACAC TAACTGCCTG AATTATTAGT CTGCCTCAGG ACTATCTTAA TAGTCTTCGC	2295
AAGGTTGTTT TGAGATTAA TTAGATAGGA GTTCCTGTCT AGGCGCGACG GAAACAGATC	2355
CGACTCAGAA CCATGAGACA GGTTCGATCC CTGGCTTTGT CAGTGGGTTA GGATCTGGTG	2415
CTGCTGTGAG CTGTGGTGTA GGTGCGCAGAG GTGGCTCGGA TCCCGCGTTG CTGTGGCTGT	2475
GGTGTAGGCC GGTGCAGACA GCTCCGATTA GACCCCTAGC CTGGGAACCT CCATGTGCCG	2535
CGGGTACCGC TAAAAAAGA CAAAAGATGG AAAAAAAAAA GGTTACATTA GATAAAGCAA	2595
GTGACTCCTC CACCACCACA CATATCCCTG CAGAACCAGG ACAGAGCATG CCTTCTTGAA	2655
AAGTTTTCGG TTGTGGCTTT GATAGCACCC AGCCTTAAAA GCCAGCTTTT CAATCTGCCC	2715
AGAGCAGTCT GGAGACTTCC GCATCTCCTG GCCACTCTGA GTTTCTAACA GTGGCCTTGG	2775
CGAGCCTGGG AGCAGTCCGG TGGCCAGAAG CAGGGACAGC TGAGAACCAG ATAGAGTCTT	2835
GGCACTTTCA AGAGAAAACC CTAAGTCTCC TTCTTCCAGC CATGCAACAG CTGCGCATGA	2895
CAGATCCAGC GTGTCCCAGC CTGTGTGGTG CAGGGAGTGA YGCTGCGNNY AGGGYGYGGG	2955
GGAGCTGAGG AGCGAGGCGG GGCATCGNGG GGCTGCAGCC TCCATCCCTA AGTGGGGAGA	3015
CTTCATGAAG AGCCTGACCA GNAGGGAGGG GCATGTGTGG AGGACCTCAG GGCCTGGGGA	3075
AGGCTAGACC CAACTATGTG AGAAACAGAC AGTCGTGGCT GGTTCTACAG AAGAGGCATC	3135
TGGAGGCCAT TCGAATGCCC AAAGCTGTCT GGGTGAGGCA GGGCTTGCTA GGCAGAAGAC	3195
AGAAGGCCGT GAGACCAGCT TGGAGGCTTG GCAGCCACGC CAGCCCAAGG AGTTCGGGCC	3255
TAGATAGGAT TGTGTGGAAG GGAAGAGGC AGCCGGAGGT GGGGGGTGGG GGTGGACCCG	3315
TCTCCACGCC TGCAGGAAGG CCAGGGGCTG CAGAGCCAAC ATCTCTCTCG CTGAGCGTCT	3375
CGCTCTCCCC TTCCTCCTGC ACAG CAG TCT GTC TCC TCC AAA CAG AGG GTC	3426
Gln Ser Val Ser Ser Lys Gln Arg Val	
50 55	
ACC GGT TTG GAC TTC ATC CCT GGG CTC CAT CCT GTC CTG AGT TTG TCC	3474
Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Val Leu Ser Leu Ser	
60 65 70	
AAG ATG GAC CAG ACC CTG GCG ATC TAC CAA CAG ATC CTC ACC AGT CTG	3522
Lys Met Asp Gln Thr Leu Ala Ile Tyr Gln Gln Ile Leu Thr Ser Leu	
75 80 85	

CCT TCC AGA AAT GTG ATC CAA ATA TCG AAT GAC CTG GAG AAC CTC CGG	3570
Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg	
90 95 100 105	
GAC CTT CTC CAC CTG CTG GCC TCC TCC AAG AGC TGC CCC TTG CCC AGC	3618
Asp Leu Leu His Leu Leu Ala Ser Ser Lys Ser Cys Pro Leu Pro Ser	
110 115 120	
AGG GCC CTG GAG ACC TTG GAG AGC CTG GGC GGC GTC CTG GAA GCC TCC	3666
Arg Ala Leu Glu Thr Leu Glu Ser Leu Gly Gly Val Leu Glu Ala Ser	
125 130 135	
CTC TAC TCC ACG GAG GTG GTG GCC CTG AGC AGG CTG CAG GGG GCT CTG	3714
Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln Gly Ala Leu	
140 145 150	
CAG GAC ATG CTG CGG CAG CTG GAC CTC AGC CCT GGC TGC TGAAGCCTTG	3763
Gln Asp Met Leu Arg Gln Leu Asp Leu Ser Pro Gly Cys	
155 160 165	
AAGGCCTCTC TCCCCACAGT CGGGGGAAGA AACCTGAGCT TCCAGGAGTC TGCTGGAGAA	3823
GAGAGCCTGT GCGGACCTCC TCTCTGCAGG TCTGCGGACC ATTTCTCTCT CGCTCCGCTA	3883
AGCTGCTCTT CCAAAGGCAG AAAACTCCAA GGCACGACAC CAAAGACAGA AAGGCCTGGT	3943
TCCGCGCCCA CCGGAAAGGG GGCGCCGTCC AGCCAACGGT GGACTIONATT TCGATTTTTC	4003
CACCAACGTC TTCCTTCCTG TTCCATCTCC AGCTCACCGC GTGCTTCAGC GTGACCGGGG	4063
GGATTTTACA GCCTTTTCGAC CATCAAGCAG GGTTCATCT GAGAATTCCG GGGAGCACGG	4123
TGAAGGCTAC AGGCACACAC AGCTGGATGC TCCCACGCAA CACAAGTTGG AAGCATTCT	4183
TTATTTATTA TGCGGTGTAT TCTGGTTGGA TTTGAAGCAA AACACCAGCC TTTCCAGGCT	4243
CTCTGGGGTC AGCCGGGGCT AGGGGGAGGC TCCCGAGGTG CTGTTTCCAG TACCATCCAT	4303
GGGCTGTCTG AGGCCAACCC ATTTTGAGTG ACTTGAGGGC TCTCAAGGTC GTTCTCTAGA	4363
GACTIONTTTT GTTTCTACTG TGACTIONTT TAAAACTGCA GCGTGTGCAC TGGCATCGCC	4423
TGCGCGGATC TCGAAGGGCC AGGTTCTCTT AGAAAGAAGA AGATGACTIONT TGTCAGGGGT	4483
GTGTACCGG AGACAGGAAG TGTGTTGGTG GCGGGGGCAT GGATCCAGAA TGTGTATTTT	4543
TTGTGTGATG GACATTTGTG TGAGGGGCTC TCTGGACAGG GTGAGGTCAT TGTCTCATCT	4603
TCGTGGTTTT CATGAGAGAA GGAGATGATT CCTTCACGGG GGTCGTGGGG TTTTGCCAGC	4663
CGCCCGTGCA GGAGTGGGGA AGGGGCTGAA GCCGAAGACC GTTGGGGGCC GTGGTGAGCT	4723
CTGCCTTCTC CAGCTGCTAG AGGCTGGTCT TTCTCATCAG GGAGTGAGGG TCTCGCGTTG	4783
GAGACAGTGA TCCCCAGGGC GGGATCCTTG CCGTGCCCT CTGAATGGTC TGGGTGATCC	4843
CACACTGATG TCATAACAGG GAAGTGCCCT GGTTTGGGAT TTGTATGCTC ACCCAAAGCA	4903
AGGGCTGTCT TCCCATCCAT TTTGGGAAGG ATTTTTTCTC CAGGGGGAGG GTGAAAGCTC	4963
TGGGAGGTCT GTGGGCTTAC GAGATGGTCC AAGTCCTGGG TCAGTGAGTC CCGGGACTCG	5023
TGACCGCCTC GAGGAGCCCC CTTCTCCCTA CAGGTCATGT TCAATAGGTC AAACAAGGAG	5083

GCATGGGTTT CCACCATCCT GCCGCTGTGA TGCAGCCATC GCACTACAGG AGGTAGATCT	5143
GTCCAAGGAA ATTTGAATCT CAAGCAATCA CTTTCAAGAC TGAGCATCTA TTGTGCTCAG	5203
CCCCAACTGG TGCTATGGGC TCAGAGAAGC TCATCAAATA AATATTAAAA TCCAGTCCTG	5263
CCTTCAGGAC CTTGCATTCC AGATGATAAC ACCTCCCCCA CACCCCGTCT GCAGAGGCTG	5323
TCATTTACC ATGGCAACCG AGCAGCTGAA ACACAGTGCG GTCCTCAGCA GGTGGAAAGG	5383
CTGAGCTGAG GAGGGCAGTG CCCGGGCCCCA CAGGCTAACC CTGCTTGAC TTGGTAGCAT	5443
TTTTACTGTT CGGGGCGCAT CAGCATCTAT TACTGAGAAG CCGCATCCCT TTGAAGCAGG	5503
ATAGCTGAGA CTATAAAAT AAGAAAATAC CAGAGTCCC TTGTGGCACA GAGGGCTAAG	5563
GATCCAGTGT TGTGCTGCA GCAGCTTGGG TCACGGCTGT GGCAAGGGTT CGATCCCTGG	5623
CCTGGGAACT TTCACATGTT GCAGGCAAGG CCAAAAAAAAA ATAAATAAAT AAAAATAAAC	5683
AAAAAAAAAAC AAGACCATAA CAGCAGACTG GTGGCAAACC AGGACTAGAA CCTGGGTCCT	5743
CTGACCCCTA GAGTCAGTGT CCCCTGAGCC AGCTAGTGTT CTCTGGGGAC GGGAACAGGG	5803
TTGGGCAGGG AGTTCAGGAA GTGTTTGCTG GAAGAGCGGA GTTTCAGGC TGATTTTGCA	5863
GGAGGTGAGG GAAGTGGATT GCCTGGAGGG AGGAGGCTGT TTTGTTTGAA GCTT	5917

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Cys	Gly	Pro	Leu	Cys	Arg	Phe	Leu	Leu	Ala	Leu	Ala	Tyr	Leu
1					5				10					15	
Ser	Tyr	Val	Glu	Ala	Val	Pro	Ile	Trp	Arg	Val	Gln	Asp	Asp	Thr	Lys
			20					25					30		
Thr	Leu	Ile	Lys	Thr	Ile	Val	Thr	Arg	Ile	Ser	Asp	Ile	Ser	His	Met
		35					40					45			
Gln	Ser	Val	Ser	Ser	Lys	Gln	Arg	Val	Thr	Gly	Leu	Asp	Phe	Ile	Pro
		50				55					60				
Gly	Leu	His	Pro	Val	Leu	Ser	Leu	Ser	Lys	Met	Asp	Gln	Thr	Leu	Ala
	65				70					75				80	
Ile	Tyr	Gln	Gln	Ile	Leu	Thr	Ser	Leu	Pro	Ser	Arg	Asn	Val	Ile	Gln
				85					90					95	
Ile	Ser	Asn	Asp	Leu	Glu	Asn	Leu	Arg	Asp	Leu	Leu	His	Leu	Leu	Ala
		100						105					110		
Ser	Ser	Lys	Ser	Cys	Pro	Leu	Pro	Ser	Arg	Ala	Leu	Glu	Thr	Leu	Glu
		115						120					125		

Ser Leu Gly Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val
 130 135 140

Ala Leu Ser Arg Leu Gln Gly Ala Leu Gln Asp Met Leu Arg Gln Leu
 145 150 155 160

Asp Leu Ser Pro Gly Cys
 165

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 435 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTG CCC ATC TGG AGA GTC CAG GAT GAC ACC AAA ACC CTC ATC AAG ACG	48
Val Pro Ile Trp Arg Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr	
1 5 10 15	
ATT GTC ACC AGG ATC AGT GAC ATT TCA CAC ATG CAG TCT GTC TCC TCC	96
Ile Val Thr Arg Ile Ser Asp Ile Ser His Met Gln Ser Val Ser Ser	
20 25 30	
AAA CAG AGG GTC ACC GGT TTG GAC TTC ATC CCT GGG CTC CAT CCT GTC	144
Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Val	
35 40 45	
CTG AGT TTG TCC AAG ATG GAC CAG ACC CTG GCG ATC TAC CAA CAG ATC	192
Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Ile Tyr Gln Gln Ile	
50 55 60	
CTC ACC AGT CTG CCT TCC AGA AAT GTG ATC CAA ATA TCG AAT GAC CTG	240
Leu Thr Ser Leu Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu	
65 70 75 80	
GAG AAC CTC CGG GAC CTT CTC CAC CTG CTG GCC TCC TCC AAG AGC TGC	288
Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Ser Ser Lys Ser Cys	
85 90 95	
CCC TTG CCC AGC AGG GCC CTG GAG ACC TTG GAG AGC CTG GGC GGC GTC	336
Pro Leu Pro Ser Arg Ala Leu Glu Thr Leu Glu Ser Leu Gly Gly Val	
100 105 110	
CTG GAA GCC TCC CTC TAC TCC ACG GAG GTG GTG GCC CTG AGC AGG CTG	384
Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu	
115 120 125	
CAG GGG GCT CTG CAG GAC ATG CTG CGG CAC GTG GAC CTC AGC CCT GGC	432
Gln Gly Ala Leu Gln Asp Met Leu Arg His Val Asp Leu Ser Pro Gly	
130 135 140	

TGC
Cys
145

435

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Val Pro Ile Trp Arg Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr
 1           5           10           15
Ile Val Thr Arg Ile Ser Asp Ile Ser His Met Gln Ser Val Ser Ser
          20           25           30
Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Val
          35           40           45
Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Ile Tyr Gln Gln Ile
          50           55           60
Leu Thr Ser Leu Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp Leu
          65           70           75           80
Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Ser Ser Lys Ser Cys
          85           90           95
Pro Leu Pro Ser Arg Ala Leu Glu Thr Leu Glu Ser Leu Gly Gly Val
          100          105          110
Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu
          115          120          125
Gln Gly Ala Leu Gln Asp Met Leu Arg His Val Asp Leu Ser Pro Gly
          130          135          140
Cys
145
```

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 504 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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ATGCATTGGG GAACCCTGTG CGGATTCTTG TGGCTTTGGC CCTATCTTTT CTATGTCCAA      60
GCTGTGCCCA TCCAAAAAGT CCAAGATGAC ACCAAAACCC TCATCAAGAC AATTGTCAACC      120
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AGGATCAATG ACATTTTACA CACGCAGTCA GTCTCCTCCA AACAGAAAGT CACCGGTTTG	180
GACTTCATTC CTGGGCTCCA CCCCATCCTG ACCTTATCCA AGATGGACCA GACTCTGGCA	240
GTCTACCAAC AGATCCTCAC CAGTATGCCT TCCAGAAACG TGATCCAAAT ATCCAACGAC	300
CTGGAGAACC TCCGGGATCT TCTTCACGTG CTGGCCTTCT CTAAGAGCTG CCACTTGCCC	360
TGGGCCAGTG GCCTGGAGAC CTTGGACAGC CTGGGGGGTG TCCTGGAAGC TTCAGGCTAC	420
TCCACAGAGG TGGTGGCCCT GAGCAGGCTG CAGGGGTCTC TGCAGGACAT GCTGTGGCAG	480
CTGGACCTCA GCCCTGGGTG CTGA	504

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGTGCTGGA GACCCCTGTG TCGGTTCTTG TGGCTTTGGT CCTATCTGTC TTATGTTCAA	60
GCAGTGCTTA TCCAGAAAGT CCAGGATGAC ACCAAAACCC TCATCAAGAC CATTGTCAAC	120
AGGATCAATG ACATTTTACA CACGCAGTCG GTATCCGCCA AGCAGAGGGT CACTGGCTTG	180
GACTTCATTC CTGGGCTTCA CCCCATCTTG AGTTTGTTCA AGATGGACCA GACTCTGGCA	240
GTCTATCCAC AGGTCCTCAC CAGCCTGCCT TCCCAAAATG TGCTGCAGAT AGCCAATGAC	300
CTGGAGAATC TCCGAGACCT CCTCCATCTG CTGGCCTTCT CCAAGAGCTG CTCCCTGCCT	360
CAGACCAGTG GCCTGCAGAA GCCAGAGAGC CTGGATGGCG TCCTGGAAGC CTCACTCTAC	420
TCCACAGAGG TGGTGGCTTT GAGCAGGCTG CAGGGCTCTC TGCAGGACAT TCTTCAACAG	480
TTGGATGTTA GCCCTGAATG CTGA	504

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGATCCGGTC TCAGGCCGTG CCYATCCARA AAGTCC	36
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(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCAGCG CTGCAYYCAG GGCTRASRTC

30